

SUBSTITUTE SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Coleman, Roger
 Au-Young, Janice
 Bandman, Olga
 Seilhamer, Jeffrey J.

(ii) TITLE OF THE INVENTION: A C5a-LIKE SEVEN TRANSMEMBRANE RECEPTOR

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 (B) STREET: 3174 Porter Drive
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/462,355
 (B) FILING DATE: June 5, 1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy .
 (B) REGISTRATION NUMBER: 36,749
 (C) REFERENCE/DOCKET NUMBER: PF-0040 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
 (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(I) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Mast Cell
 (B) CLONE: 8118

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

a2

ATGGCGTCTT TCTCTGCTGA GACCAATTCA ACTGACCTAC TCTCACAGCC ATGGAATGAG	60
CCCCCAGTAA TTCTCTCCAT GGTCAATTCTC AGCCTTACTT TTTTACTGGG ATTGCCAGGC	120
AATGGGCTGG TGCTGTGGGT GGCTGGCCTG AAGATGCAGC GGACAGTGAA CACAATTTGG	180
TTCTCTCACC TCACCTTGGC GGACCTCCTC TGCTGCCTCT CTTTGGCCTT CTCGCTGGCT	240
CACTTGGCTC TCCAGGGACA GTGGCCCTAC GGCAGGTTCC TATGCAAGCT CATCCCCTCC	300
ATCATTGTCC TCAACATGTT TGGCAGTGTC TTCCTGCTTA CTGCCATTAG CCTGGATCGC	360
TGTCTTGTGG TATTCAAGCC AATCTGGTGT CAGAATCATC GCAATGTAGG GATGGCCTGC	420
TCTATCTGTG GATGTATCTG GGTGGTGGCT TTTGTGTTGT GCATTCCTGT GTTCGTGTAC	480
CGGGAAATCT TCACTACAGA CAACCATAAT AGATGTGGCT ACAAATTTGG TCTCTCCAGC	540
TCATTAGATT ATCCAGACTT TTATGGGGAT CCACTAGAAA ACAGGTCTCT TGAAAACATT	600
GTTCAGCCGC CTGGAGAAAT GAATGATAGG TTAGATCCTT CCTCTTTCCA AACAAATGAT	660
CATCCTTGGA CAGTCCCCAC TGTCTTCCAA CCTCAAACAT TTCAAAGACC TTCTGCAGAT	720
TCACTCCCTA GGGGTTCTGC TAGGTTAACA AGTCAAAAATC TGTATTCTAA TGTATTTAAA	780
CCTGCTGATG TGGTCTCACC TAAAATCCCC AGTGGGTTTC CTATTGAAGA TCACGAAACC	840
AGCCCACTGG ATAACCTCTGA TGCTTTTCTC TCTACTCATT TAAAGCTGTT CCCTAGCGCT	900
TCTAGCAATT CCTTCTACGA GTCTGAGCTA CCACAAGGTT TCCAGGATTA TTACAATTTA	960
GGCCAATTCA CAGATGACGA TCAAGTGCCA ACACCCCTCG TGGCAATAAC GATCACTAGG	1020
CTAGTGGTGG GTTTCCTGCT GCCCTCTGTT ATCATGATAG CCTGTTACAG CTTCAATTGTC	1080
TTCCGAATGC AAAGGGGGCCG CTTGCCAAG TCTCAGAGCA AAACCTTTTCG AGTGGCCGTG	1140
GTGGTGGTGG CTGTCTTTCT TGTCTGCTGG ACTCCATACC ACATTTGGGG AGTCCTGTCA	1200
TTGCTTACTG ACCCAGAAAC TCCCTTGGGG AAAACTCTGA TGTCTTGGGA TCATGTATGC	1260
ATTGCTCTAG CATCTGCCAA TAGTTGCTTT AATCCCTTCC TTTATGCCCT CTTGGGGAAA	1320
GATTTTAGGA AGAAAGCAAG GCAGTCCATT CAGGGAATTC TGGAGGCAGC CTTCAAGTGA	1380
GAGCTCACAC GTTCCACCCA CTGTCCCTCA AACAATGTCA TTTAGAAAG AAATAGTACA	1440
ACTGTG	1446

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Phe Ser Ala Glu Thr Asn Ser Thr Asp Leu Leu Ser Gln
1 5 10 15
Pro Trp Asn Glu Pro Pro Val Ile Leu Ser Met Val Ile Leu Ser Leu
20 25 30
Thr Phe Leu Leu Gly Leu Pro Gly Asn Gly Leu Val Leu Trp Val Ala
35 40 45
Gly Leu Lys Met Gln Arg Thr Val Asn Thr Ile Trp Phe Leu His Leu
50 55 60
Thr Leu Ala Asp Leu Leu Cys Cys Leu Ser Leu Ala Phe Ser Leu Ala
65 70 75 80
His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys
85 90 95
Leu Ile Pro Ser Ile Ile Val Leu Asn Met Phe Gly Ser Val Phe Leu
100 105 110
Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Val Val Phe Lys Pro Ile
115 120 125
Trp Cys Gln Asn His Arg Asn Val Gly Met Ala Cys Ser Ile Cys Gly
130 135 140
Cys Ile Trp Val Val Ala Phe Val Leu Cys Ile Pro Val Phe Val Tyr
145 150 155 160
Arg Glu Ile Phe Thr Thr Asp Asn His Asn Arg Cys Gly Tyr Lys Phe
165 170 175
Gly Leu Ser Ser Ser Leu Asp Tyr Pro Asp Phe Tyr Gly Asp Pro Leu
180 185 190
Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn
195 200 205
Asp Arg Leu Asp Pro Ser Ser Phe Gln Thr Asn Asp His Pro Trp Thr
210 215 220
Val Pro Thr Val Phe Gln Pro Gln Thr Phe Gln Arg Pro Ser Ala Asp
225 230 235 240
Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser
245 250 255
Asn Val Phe Lys Pro Ala Asp Val Val Ser Pro Lys Ile Pro Ser Gly
260 265 270
Phe Pro Ile Glu Asp His Glu Thr Ser Pro Leu Asp Asn Ser Asp Ala
275 280 285
Phe Leu Ser Thr His Leu Lys Leu Phe Pro Ser Ala Ser Ser Asn Ser
290 295 300

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a²

Phe Tyr Glu Ser Glu Leu Pro Gln Gly Phe Gln Asp Tyr Tyr Asn Leu
305 310 315 320

Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile
325 330 335

Thr Ile Thr Arg Leu Val Val Gly Phe Leu Leu Pro Ser Val Ile Met
340 345 350

Ile Ala Cys Tyr Ser Phe Ile Val Phe Arg Met Gln Arg Gly Arg Phe
355 360 365

Ala Lys Ser Gln Ser Lys Thr Phe Arg Val Ala Val Val Val Val Ala
370 375 380

Val Phe Leu Val Cys Trp Thr Pro Tyr His Ile Trp Gly Val Leu Ser
385 390 395 400

Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp
405 410 415

Asp His Val Cys Ile Ala Leu Ala Ser Ala Asn Ser Cys Phe Asn Pro
420 425 430

Phe Leu Tyr Ala Leu Leu Gly Lys Asp Phe Arg Lys Lys Ala Arg Gln
435 440 445

Ser Ile Gln Gly Ile Leu Glu Ala Ala Phe Ser Glu Glu Leu Thr Arg
450 455 460

Ser Thr His Cys Pro Ser Asn Asn Val Ile Ser Glu Arg Asn Ser Thr
465 470 475 480

Thr Val

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAAGACAGC CACCACCACC ACG

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGAAAGCAAG GCAGTCCATT CAGG

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

a2

Met	Asn	Ser	Phe	Asn	Tyr	Thr	Thr	Pro	Asp	Tyr	Gly	His	Tyr	Asp	Asp
1				5					10					15	
Lys	Asp	Thr	Leu	Asp	Leu	Asn	Thr	Pro	Val	Asp	Lys	Thr	Ser	Asn	Thr
			20					25					30		
Leu	Arg	Val	Pro	Asp	Ile	Leu	Ala	Leu	Val	Ile	Phe	Ala	Val	Val	Phe
		35					40					45			
Leu	Val	Gly	Val	Leu	Gly	Asn	Ala	Leu	Val	Val	Trp	Val	Thr	Ala	Phe
	50					55					60				
Glu	Ala	Lys	Arg	Thr	Ile	Asn	Ala	Ile	Trp	Phe	Leu	Asn	Leu	Ala	Val
65					70					75					80
Ala	Asp	Phe	Leu	Ser	Cys	Leu	Ala	Leu	Pro	Ile	Leu	Phe	Thr	Ser	Ile
				85					90					95	
Val	Gln	His	His	His	Trp	Pro	Phe	Gly	Gly	Ala	Ala	Cys	Ser	Ile	Leu
			100					105					110		
Pro	Ser	Leu	Ile	Leu	Leu	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	Leu	Ala
		115					120					125			
Thr	Ile	Ser	Ala	Asp	Arg	Phe	Leu	Leu	Val	Phe	Lys	Pro	Ile	Trp	Cys
	130					135					140				
Gln	Asn	Phe	Arg	Gly	Ala	Gly	Leu	Ala	Trp	Ile	Ala	Cys	Ala	Val	Ala
145					150					155					160
Trp	Gly	Leu	Ala	Leu	Leu	Leu	Thr	Ile	Pro	Ser	Phe	Leu	Tyr	Arg	Val
				165					170					175	
Val	Arg	Glu	Glu	Tyr	Phe	Pro	Pro	Lys	Val	Leu	Cys	Gly	Val	Asp	Tyr
		180						185					190		
Ser	His	Asp	Lys	Arg	Arg	Glu	Arg	Ala	Val	Ala	Ile	Val	Arg	Leu	Val
		195					200					205			
Leu	Gly	Phe	Leu	Trp	Pro	Leu	Leu	Thr	Leu	Thr	Ile	Cys	Tyr	Thr	Phe
	210					215					220				
Ile	Leu	Leu	Arg	Thr	Trp	Ser	Arg	Arg	Ala	Thr	Arg	Ser	Thr	Lys	Thr
225					230					235					240
Leu	Lys	Val	Val	Val	Ala	Val	Val	Ala	Ser	Phe	Phe	Ile	Phe	Trp	Leu
				245					250					255	
Pro	Tyr	Gln	Val	Thr	Gly	Ile	Met	Met	Ser	Phe	Leu	Glu	Pro	Ser	Ser
		260					265						270		
Pro	Thr	Phe	Leu	Leu	Leu	Asn	Lys	Leu	Asp	Ser	Leu	Cys	Val	Ser	Phe
		275					280					285			
Ala	Tyr	Ile	Asn	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Val	Val	Ala	Gly
	290					295					300				
Gln	Gly	Phe	Gln	Gly	Arg	Leu	Arg	Lys	Ser	Leu	Pro	Ser	Leu	Leu	Arg
305					310					315					320
Asn	Val	Leu	Thr	Glu	Glu	Ser	Val	Val	Arg	Glu	Ser	Lys	Ser	Phe	Thr
				325					330					335	
Arg	Ser	Thr	Val	Asp	Thr	Met	Ala	Gln	Lys	Thr	Gln	Ala	Val		
			340					345					350		